


```
Db 93 INSSGPRPPVPPSPAPGPPGSPRLRIGDQEDPSLPALIEFKIHYLDTTTLEIEVARS 152
Qy 125 RQSGSVILROEAEYVRLDFNGNDEEDLPFKKGDLIRIRDKPEQWMAAEDSEGRK 184
Db 153 RQSGSVILROEAEYVRLDFNGNDEEDLPFKKGDLIRIRDKPEQWMAAEDSEGRK 212
Qy 185 IPVPYVEKRPASASVSALIGNOEGS 211
Db 213 IPVPYVEKRPASASVSALIGNOEGS 239

RESULT 2
Q99059 PRELIMINARY; PRT; 255 AA.
ID Q99059;
AC Q99059;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GAG-CRK PROTEIN (FRAGMENT).
OS Avian sarcoma virus 1.
OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX NCBI_TaxID=11957;
RN [1]
RP MEDLINE=90045469; PubMed=2554234;
RA Tsuchie H., Chang C.H.W., Yoshida M., Vogt P.K.;
RT "A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene."
RL Oncogene 4:1281-1284(1989).
CC -1 SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.
DR EMBL: X17292; CAA35181.1; -
DR HSSP: O64010; ICKA.
DR InterPro: IPR000980; -
DR InterPro: IPR001452; -
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PSS0001; SH2; 1.
DR PROSITE: PSS0002; SH3; 1.
DR SMART: SM00326; SH3; 1.
KW Oncogene; Polyprotein; SH3 domain; SH2 domain.
FT NON_TER 1
FT DOMAIN 1
FT DOMAIN 24 23 GAG (BY SIMILARITY).
FT DOMAIN 63 112 CRK (BY SIMILARITY).
FT DOMAIN 188 239 SH2 (OR B+C BOX) (BY SIMILARITY).
FT DOMAIN 254 255 SH3 (OR A BOX) (BY SIMILARITY).
SQ SEQUENCE 255 AA; 27985 MW; 0C562DOB2327A579 CRC64;

Query Match 49.3%; Score 834.5; DB 14; Length 255;
Best Local Similarity 78.3%; Pred. No. 1.5e-61;
Matches 159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;
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RESULT 3
Q9NHC3 PRELIMINARY; PRT; 279 AA.
ID Q9NHC3;
AC Q9NHC3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE CELL-CORPSE ENGULFMENT PROTEIN CED-2.
GN CED-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Reddien P.W., Horvitz H.R.;
RT "CED-2/CrklI and CED-10/Rac control phagocytosis and cell migration in C. elegans."
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL: AF226866; AAF3845.1; -
DR InterPro: IPR000980; -
DR InterPro: IPR001452; -
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PSS0001; SH2; 1.
DR PROSITE: PSS0002; SH3; 1.
SQ SEQUENCE 279 AA; 30878 MW; 5CE7DA478948970B CRC64;
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Query Match 20.3%; Score 343; DB 5; Length 279;
Best Local Similarity 31.0%; Pred. No. 9.9e-21;
Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

Qy 8 FDSEERSMWYGRSLROEAVALLQGRHVGFLVNDSTSPGDYVLSV---SENSRVS 61
Db 6 FDPFMRSEFYFGMSREBAHKLT-GEPOVSIGFTLMDSS-RPEYSILVREADEGNAVC 63
Qy 62 HYIINSGPRPPVPPSPAPGPPGSPRLRIGDQEDPSLPALIEFKIHYLDTTTLEIEV 121
Db 64 HYLIERGEPK-----EDGTAAGVKTANOSFPDIPALNHFMKRVLTASLT--- 110
Qy 122 ASRQSGSVILROEAEYVRLDFNGNDEEDLPFKKGDLIRIRDKPEQWMAAEDSEGR 181
Db 111 -----AAKKPIIEVVGTFKFTGERETDLPFEGGERLEILSKTNQDMWEARNALGT 162
Qy 182 RGMIVPVYVE---KRPASASVSALIGNOEGSHPQPLGCPPEPPYAPQSVNTPPLRLQ- 237
Db 163 TGLVPANTYVOIOMEFHNDRTS-----KGASQSSISGSGGAERFSSASTSSDNIEL 213
Qy 238 --NGPIYAVRIQKRVNPAVDKTALEVGELVYTKINVSQWEGECNGRGHPFTHYR 295
Db 214 QRLPAKAKAVTFDRKPNAYDPTQLRVKKGGQVLYVTQKMSNMRYAELDQIGSVPHYLR 273

RESULT 4
Q9PU11 PRELIMINARY; PRT; 217 AA.
ID Q9PU11;
AC Q9PU11;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GRB2 PROTEIN.
GN GRB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RA Golaset C., Shi D.L., Boucaut J.C.;
```

"Selective inhibition of neural induction but not mesoderm induction by interfering mutants of *sem-5/grb2*." RT
 RT Submitted (DDBJ-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1723061: CARS9279.1; -.
 DR HSPSP; P29354; 1GHTU.
 DR InterPro: IPR000108; -.
 DR InterPro: IPR000980; -.
 DR InterPro: IPR001452; -.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PROSITE; PSS0001; SH2; 1.
 DR PROSITE; PSS0002; SH3; 2.
 DR SMART; SM00326; SH3; 1.
 SO SEQUENCE 217 AA; 25135 MW; 2349A68260F9D4CD CRC64;

Query Match 12.6%; Score 213; DB 13; Length 217;
 Best Local Similarity 27.4%; Pred. No. 4.3e-10;
 Matches 52; Conservative 45; Mismatches 57; Indels 36; Gaps 7;

QY 7 NPDSEERSWTWGRSLRQEAVALLOGRH-GVFLVRDSSISPGDYVLSSNSRYSHYIT 65
 Db 51 NYIEKKAHPWFFGKIPRAKAEEMIGKRDGAFILRESESAPOGDFSLSVKGNQVQHFKV 110
 QY 66 NSSGRRPPVPPSPAPPGVSPSRIRIGDQDFDLPALLEFYKIHLYDTTLIPVRSR 125
 Db 111 LRDG-----AGKFLWVVFNSLNLVLYHR-----STIS---VSRNQ 144
 QY 126 QSGSVILRQ-----EAEYVRLDFDNGNDEDLPEFKKGLILIRDKPEQWMAEDSEG 180
 Db 145 Q---TFLNDIQGVPPQPIYQALFDGPDQEDGELGFRGDTLQYVNDSPWMMWG-TCL 200
 QY 181 KRGMIPVPPY 190
 Db 201 QTGMFPPVY 210

RESULT 5
 QY9E96 PRELIMINARY; PRT; 600 AA.
 AC QY9E96;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE CG7129 PROTEIN.
 GN CG7129.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cackley E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harits N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon S., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wattarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh K.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03721; AAP5531.1; -.
 DR HSPSP; P29354; 1GFC.
 DR FlyBase: FBgn0038599; CG7129.
 DR InterPro: IPR000108; -.
 DR InterPro: IPR001452; -.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PROSITE; PSS0002; SH3; 2.
 DR SMART; SM00326; SH3; 1.
 SO SEQUENCE 600 AA; 62961 MW; 9E3EA36C4A165A3 CRC64;

Query Match 11.8%; Score 200; DB 5; Length 600;
 Best Local Similarity 25.4%; Pred. No. 2e-08;
 Matches 63; Conservative 35; Mismatches 90; Indels 60; Gaps 8;

QY 61 SHYIINSSGRRPPVPPSPAPPGVSPSRIRIGDQDFDLPALLEFYKIHLYDTTLIP 120
 Db 396 SGVAGSTPPSPWPKGPPPPPPASSGGSILDDYNGKDAL-----A 439
 QY 121 VARSQSGVILRQEAVALLOGRH-GVFLVRDSSISPGDYVLSSNSRYSHYIT 180
 Db 440 LSNCGG---YMEEEVPPVAVVLDGPDGIPGDLSPREGEKTYLLDHPPEWLRGRTBSG 496
 QY 181 KRGMIPVPPVPPVPPSPAPPGVSPSRIRIGDQDFDLPALLEFYKIHLYDTTLIP 240
 Db 497 CEGIFPPVYVDIKVPLGAT-----GGAAPATASMAAPSPSS----- 534
 QY 241 IYAVNIDKRVPMX-----DKTALALEVGLVYKTKLVNSGOW-EGSCNKRGRHFP 291
 Db 535 -----QQQLPTALCLYHPGEVEGDLAQENELVTL-YRINEDMLYGEVARGQGF 506
 QY 292 THVRILDD 299
 Db 587 --ANFLDD 592

RESULT 6
 QY9H06 PRELIMINARY; PRT; 1067 AA.
 AC QY9H06;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE PHOSPHOLIPASE C-GAMMA-1B (FRAGMENT).
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; *Xenopus*.


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QY 122 ABRQSSGTYILNQEAEE-----VALDFFNGNNEEDLPKRDITLRIDPK 168
DQ 558 GTPDPDYGALYEGRNPRGVEYVIANMPTFKCSVRALLDYKAQREDEBLFTTKNTLIQNEKO 617
QY 169 EEDQNNAAEESSEKRCM-LPRVYVEK-RRASASVSLYLIGNEGSHRPLGSEPRGUYAO 226
DQ 618 EGGHMGG-DCGGRKKMMWPFANMIMELTSP-----PPEPERO 653
QY 227 P-SVNTPLPFLNONG 239
DQ 654 HLDENSPGLDILGG 667

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RESULT	8		
ID	090279	PRELIMINARY;	PRT; 1097 AA.
AC	090279;		
DT	01-MAY-2000 (TEMBLrel. 13, Created)		
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)		
DT	01-MAY-2001 (TEMBLrel. 16, Last annotation update)		
DE	Y116A8C.36 PROTEIN.		
GN	Y116A8C.36		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditiidae; Pelodierinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	McMurray A.A.;		
RL	Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	none;		
RX	MEDLINE=99069613; PubMed=9851916;		
RT	"genome sequence of the nematode C.elegans: A platform for		
RT	investigating biology.";		
RL	Science 282:2012-2018(1998).		
CC	-1- SIMILARITY: TO EF-HAND FAMILY.		
DR	EMBL; AL117204; CAB55138.1; -.		
DR	HSSP; P29355; ISEM.		
DR	InterPro; IPR000108; -.		
DR	InterPro; IPR000194; -.		
DR	InterPro; IPR000261; -.		
DR	InterPro; IPR001452; -.		
DR	InterPro; IPR002048; -.		
DR	Pfam; PF000018; SH3.5.		
DR	Pfam; PF000036; efhand.2.		
DR	PRINTS; PR00499; P67PHOX.		
DR	PRINTS; PR00452; SH3DOMAIN.		
DR	PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.		
DR	PROSITE; PS000018; EF_HAND; UNKNOWN_2.		
DR	PROSITE; PSS00002; SH3.5.		
DR	SMART; SM00054; ERF; 1.		
DR	Calcium-binding.		
DR	SEQUENCE 1097 AA; 122071 MW; 1C2BA5F103968372 CRC64;		

	Oneiryl Match	10.8%;	Score 182;	DB 5;	Length 1097;
	Best Local Similarity	21.2%;	Pred. No. 1,4e-06;		
	Matches 75;	Conservative 56;	Mismatches 144;	Indels 78;	Gaps 14;
OY	6 GNPDSERSRSMY---MGRLSRQEAVA-LLOCGRH-----GVFLVRS-----				43
	: : :				
Db	627 GEFPKTDASGRFPADGATGTADPPAQIQAQAPAHSKGANVDQSALNIHDYTKCALRAFEA				686
OY	44 -----STSPGDYVLVSSENS-----RVSHY-----INSSGPRPVVP				76
	: : : : :				
Db	687 RSEDELSFEEDGYIIIFOSHAAEPGWRAGOLREKVGWPEAFPAIAAVPTPGCDPPIGN				746
OY	77 SPNAPPYGVSPLRKIGDDEFDSLALLEFYKIHLDTTLIEVANSRGSGSVILRQE				136
	- - - - -				
Db	747 MPNMPTSSSDVIDIGKAARKAEIAAA-----MGLTEGAPPASSAPAAAIVSQCI				798
	- - - - -				

QY 137 AEYRALFEDNGENEDDLPFKKQILTRLRPKPEOMMWNDESEGRKMIPIVPEYEXRPA 196
 Db 799 AQ-----FQMRARNEDDLSFAKGPOTIELEK-QEMMKGRNPNAGELGMFPRSYKKEVGAT 852
 QY 197 SASVSAALIGDNGESHPPGLGPERGTYAAPS---NTPLPMLOKNP---TYAAVIQKRV 250
 Db 853 TSTTTPVPSKSKSA-----GAPGMAAQDYDVPSDYTLQASLPAFOOLLYTYDF-- 905
 QY 251 PMAYDKTALALEYGELVKYTKINSGWEEBCNGKRGHPFTTHVRLDQONPD 303
 Db 906 -EAETTDALHAGDTITVLEKN-DEMMKGCGRGSEIPNAYVEISVQAQGD 956

RESULT	9		
ID	060593	PRELIMINARY;	PRT; 640 AA.
AC	060593;		
DT	01-AUG-1998 (TrEMBLrel. 07, Created)		
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	ARG/ABL-INTERACTING PROTEIN ARGBP2B (FRAGMENT).		
GN	ARGBP2B.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97362243; PubMed=9211900;		
RA	Wang B., Golemis F.A., Kruih G.D.;		
RT	ArgB2B, a multiple Src homology 3 domain-containing, Arg/Abi-		
RT	interacting protein, is phosphorylated in v-Abl-transformed cells and		
RT	localized in stress fibers and cardiolocyte Z-disks.";		
RL	J. Biol. Chem. 272:17542-17550(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Wang B., Golemis F.A., Kruih G.D.;		
RL	Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.		
EMBL	AF049885; AAC05509.1; -.		
DR	HSSP; P29354; 1GRI.		
DR	InterPro; IPRO00108; -.		
DR	InterPro; IPRO01452; -.		
DR	InterPro; IPRO02965; -.		
DR	InterPro; IPRO03127; -.		
DR	Pfam; PF00018; SH3; 2.		
DR	Pfam; PF02208; SorB; 1.		
DR	PRINTS; PRO0499; P67PHOX.		
DR	PRINTS; PRO1217; PRICEXTENSN.		
DR	PRINTS; PRO0452; SH3DOMAIN.		
DR	PROSITE; PSS0002; SH3; 2.		
DR	SMART; SM00326; SH3; 1.		
FT	NON_TER 640 640		
SO	SEQUENCE 640 AA; 70660 MW; 030AB5C053631674 CRC64;		

Query Match	10.2%	Score 173;	DB 4;	Length 640;
Best Local Similarity	26.0%	Pred. No. 3,7e-06;		
Matches	72;	Conservative	29;	Mismatches 92; Indels 84; Gaps 12;
OY	43	SSISPGDIYLSVSENSRVSHIYINNSGPPPPYPPSPAAPP-----	PGVSPSLRLIG	93
Db	393	SRTPSGRVDLPGSSITLTKSF--TSSSPSPSKAKDRSPSSYSTLTMDGKSPAPRRERG		450
OY	94	DOEFDSPALLAEFYKITHYIDTTLLIEPVARSKOGSGVILROEAEVYRALFPDNGDEED		153
Db	451	TPREKRLPA-----	KAVYDEKQTSKE	472
OY	154	LPEKKGILILIRKPREQMMNADESKRGKIPVYVEKYKRPASASVALIGNOGSGNP		213
Db	473	LSFKKSGVTLIRKIDNNMTEGE-HHGRGILPISIVYEKLTP-----		513
OY	214	QPLGPGPEGAYADPSVNTPLPNLQNGPIYARVYLOKRFVNAYDKTALALEVGEELVVKTKIN		273

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Db 514 -----PEK---AOPA--RPPPAQPEI-GEAIKYNFNADTNVELSRKGDVILLK-R 561
QY 274 VSGOM-EGECNG--KRGHFPPTHVRLDQOND-EDF 306
Db 562 VDNWMEGKIPIGTNRQIGFIPVSVKVKNTKGAEDY 598

RESULT 10
ID 060592 PRELIMINARY: PRT: 666 AA.
AC 060592;
DT 01-AUG-1998 (TRENBLREL. 07, Created)
DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)
DE 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE ARG/ABL-INTERACTING PROTEIN ARGBP2A.
GN ARGBP2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=97362243; PubMed=9211900;
RA Wang B., Golemis E.A., Krub G.D.;
RT "ArgBP2, a multiple Src homology 3 domain-containing, Arg/ABL-
RT interacting protein, is phosphorylated in v-ABL-transformed cells and
RT localized in stress fibers and cardiocyte Z-disks.";
RL J. Biol. Chem. 272:17542-17550(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Wang B., Golemis E.A., Krub G.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049884; AAC05508.1; -.
DR HSSP; P29354; IGR1.
DR InterPro; IPR001452; -.
DR InterPro; IPR003127; -.
DR Pfam; PF00018; SH3; 3.
DR Pfam; PF02208; Sortb; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRODOM; PD016158; -. 1.
DR PROSITE; PS50002; SH3; 3.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 666 AA; 74803 MW; B549A26DC04782E0 CRC64;

Query Match 10.2%; Score 173; DB 4; Length 666;
Best Local Similarity 26.0%; Pred. No. 3.9e-06;
Matches 72; Conservative 29; Mismatches 92; Indels 84; Gaps 12;

QY 43 SSTSPGDYVLSVSENSRVSHYIINSSGPRPVPSPAPQPP-----PGVSPSRRLRG 93
Db 368 SRSPSPGVLDLPGSSSTLTLSF--TSSSPSPBRADRESPRYSSTLMDGRSAPRERGG 425
QY 94 DQEPDSLPALEFYKIHVLDITTLIEPVARSQSGVILRQEAAYVALDFNGNDEED 153
Db 426 TPKEKELPA-----KAYVDFKQTSKE 447
QY 154 LPFKGDLIRDKPEOMNNAEDSEGRKGMIPVYVEKYPASASVALIGNQEGSHP 213
Db 448 LSRKGDVYIILKIDQNMTEGE-HHGRVGIPISTYVELTP----- 488
QY 214 QPLGPEPGPVAPSVNTPPLNLQNGPIYARVIOKRVNAYDKTALALEVGLVKYTKIN 273
Db 489 -----PEK---AOPA--RPPPAQPEI-GEAIKYNFNADTNVELSRKGDVILLK-R 536
QY 274 VSGOM-EGECNG--KRGHFPPTHVRLDQOND-EDF 306
Db 537 VDNWMEGKIPIGTNRQIGFIPVSVKVKNTKGAEDY 573

RESULT 11

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Q9UFT2
ID 09UFT2 PRELIMINARY: PRT: 816 AA.
AC 09UFT2;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE HYPOTHETICAL 90.2 KDA PROTEIN.
GN DKF2P586P1422.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-UTERUS;
RA Koehler K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL117472; CAB55947.1; -.
DR HSSP; O60631; IGR0.
DR InterPro; IPR00108; -.
DR InterPro; IPR001452; -.
DR InterPro; IPR003127; -.
DR Pfam; PF00018; SH3; 3.
DR Pfam; PF02208; Sortb; 1.
DR PRINTS; PR00499; P67PHOX.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50002; SH3; 3.
DR SMART; SM00459; Sortb; 1.
KW Hypothetical protein.
SQ SEQUENCE 816 AA; 90201 MW; FFE6647DC7730D4 CRC64;

Query Match 10.0%; Score 170; DB 4; Length 816;
Best Local Similarity 25.1%; Pred. No. 9.1e-06;
Matches 69; Conservative 34; Mismatches 100; Indels 72; Gaps 12;

QY 41 RDSSTPGDYVLSVSENSRVSHYIINSSGPRP-----PVPSPPAPPGVSPSRRLRG 93
Db 501 RESDAPGD--LTSLENERQIKYSVLEGGDIPLOGLSGLRPSASSATKDESPR----- 553
QY 94 DQEPDSLPALEFYKIHVLDITTLIEPVARSQSGVILRQEAAYVALDFNGNDEED 153
Db 554 -----HFIPADYLEST---EEFIRRRHD-----DKEMRRPARKFDKQATLKE 593
QY 154 LPFKGDLIRDKPEOMNNAEDSEGRKGMIPVYVEKYPASASVALIGNQEGSHP 213
Db 594 LPLQKGDVYIYKQIDQMWYEGE-HHGRVGIPISTYVELTP----- 637
QY 214 QPLGPEPGPVAPSVNTPPLNLQNGPIYARVIOKRVNAYDKTALALEVGLVKYTKIN 273
Db 638 -----AOPKILTPVOYLE---YGEAIKYNFNADTNVELSRKGDVILLK-R 681
QY 274 VSGOM-EGECNG--KRGHFPPTHVRLDQOND-EDF 306
Db 682 VDNWMEGKIPIGTNRQIGFIPVSVKVKNTKGAEDY 716

RESULT 12
ID 042287 PRELIMINARY: PRT: 1270 AA.
AC 042287;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE INTERSECTIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoffman N.G., Hardison N.L., Yamabhai M., Kay B.K.;

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Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL: AF032118; AAC73068.1; -.
 DR HSSP: P29355; ISEM
 DR InterPro: IPR000261; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR002048; -.
 DR Pfam: PF00018; SH3; 5.
 DR Pfam: PF00036; ehand; 2.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
 DR PROSITE: PS50002; SH3; 5.
 DR SMART: SM00027; EH; 1.
 DR Calcium-binding.
 SO SEQUENCE 1270 AA; 143670 MW; EA940C1F6B6A6858 CRC64;

Query Match 9.7%; Score 165; DB 13; Length 1270;
 Best Local Similarity 24.5%; Pred. No. 4.3e-05;
 Matches 75; Conservative 38; Mismatches 79; Indels 114; Gaps 18;

QY 11 EERSWVGRLRQEAVALLOGRHGVLVADSSSPGDIYLVSENSRVSHTIINSGP 70
 DB 928 EQQDKMMWFG-----VQGQK-GWP-----PKSYKLLISGLPKSTIDSTISSE 969
 QY 71 RPPVPPSPAPPPGVSPSRIRIGDQFEDSLPALLEFYKIHLYDTTTLIEPARSRQSGV 130
 DB 970 SP-----ASLKRVSAPFK-PAI-----QGE-- 989
 QY 131 ILROEAAYRALFDENGDEEDLPFKKGDILIRDKPEEQMNAEDSEGRKMIIPVYV 190
 DB 990 -----YLI-SMYEESNEGDILFQOGDIL-VVKKRKGDMWTGTVE-KTGVFPSPMYV 1039
 QY 191 EKYRPASVSVALIGNQESHPOPLGPEPGPYAQPVSNTPLPLAQGPYARIQKRV 250
 DB 1040 ---RKDSEAG--SGGTGS-----LGKKPLAQYIA--- 1067
 QY 251 PNAYDKTA---LALFVGLVYKTLINVSQWEGE--CNGKR---GHFPTVHRL---D 298
 DB 1068 --SVATAPEQTLTAPGQLILIRKKNPGRWMEGLQAGKKRQIGWFPANYVKLLSPGTN 1125
 QY 299 QONPDE 304
 DB 1126 KSTPRE 1131

RESULT 13
 ID 035413 PRELIMINARY; PRT; 1196 AA.
 AC 035413;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 15, Last annotation update)
 DE SH3-CONTAINING PROTEIN P4015.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ide N., Takeuchi M., Hata Y., Takai Y.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026505; AAB81527.1; -.
 DR HSSP: P29354; IGR1.
 DR InterPro: IPR000822; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR003127; -.
 DR Pfam: PF00018; SH3; 3.
 DR Pfam: PF02208; Sorb; 1.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRODOM: PD016158; -; 1.
 DR PROSITE: PS50002; SH3; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.

DR SMART: SM00326; SH3; 1.
 SO SEQUENCE 1196 AA; 134052 MW; 84EB1DFD64D4884 CRC64;

Query Match 9.7%; Score 164; DB 11; Length 1196;
 Best Local Similarity 29.1%; Pred. No. 4.8e-05;
 Matches 57; Conservative 31; Mismatches 70; Indels 38; Gaps 10;

QY 115 TTLIEPARSRQSGVILROEAAYRALFDENGDEEDLPFKKGDILIRDKPEEQMNA 174
 DB 942 TDLGRSVSRERRGTP---EEVKLPAKAYDFKAQTSKELSFKGGDTYILRKIDQNWYE 998
 QY 175 AEDSEGRKGMIPVYVEKTRPASASVALIGNQESHPOPLGPEPGPYAQPVSNTPLP 234
 DB 999 GE-HHGRVGIPIPSYVEKLP-----PER--AQPA--RPP 1029
 QY 235 NLONGPIYARVIOKRVPNADKTALALEVELYKTVKINVSQGW-EGECNG--KRGHFP 291
 DB 1030 PVQGEI-GEALIKYFNNAITNVELSLRKGRDILILK-RYDQMWYCKIPIGTRQGIIFY 1087
 QY 292 THVRLDQNP-DEDF 306
 DB 1088 SYVEVYKRNTRKGSDDY 1103

RESULT 14
 ID 09P7E8 PRELIMINARY; PRT; 857 AA.
 AC 09P7E8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ACTIN BINDING PROTEIN WITH SH3 DOMAINS.
 GN SPADJ60.02C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162631; CAB83085.1; -.
 DR InterPro: IPR000108; -.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR002108; -.
 DR InterPro: IPR002965; -.
 DR Pfam: PF00018; SH3; 2.
 DR Pfam: PF00241; cofilin_ADF; 1.
 DR PRINTS: PR00499; P67PHOX.
 DR PRINTS: PR01217; PRICHEXTENSN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PROSITE: PS50002; SH3; 2.
 DR SMART: SM00102; ADF; 1.
 SO SEQUENCE 857 AA; 91137 MW; 247EFA78BAE7097 CRC64;

Query Match 9.7%; Score 163.5; DB 3; Length 857;
 Best Local Similarity 23.8%; Pred. No. 3.4e-05;
 Matches 57; Conservative 35; Mismatches 87; Indels 61; Gaps 9;

QY 68 SGRRP-----VPPSPAPPPGVSPSRIRIGDQFEDSLPALLEFYKIHLYDTTTLIEPVAR 123
 DB 663 SVPGPAPAPVPEVPSVQPPAVVPEAGQLNPPVPLPBP-----DETQ--EP--- 711
 QY 124 SRQSGVILROEAAYR-----ALFDENGDEEDLPFKKGDILIRDKPEEQMNAEDSE 179
 DB 712 --QVGDVKATEHQPTKTPAIVYDYSPEEENIELEVENQIQLIEFVDGGMWLGNSK 769
 QY 180 GKRGMIIPVYEXRPPASASVALIGNQESHPOPLGPEPGPYAQPVSNTPLPLNLQNG 239

Db 770 GQCGLPSPNVE-----ITGPNETANNP-----AEPQAGCP----- 801
Qy 240 PIYARVIOKRVNAYDKTA-----LALVEGELVKTKINVSQWEGECNGKRGHPPTHV 294
Db 802 -----GKSVKAIYDYQACEDNELSFEDELIANVDCVDPNMWEGEGCHGRGLFSPNIV 854
RESULT 15
Q9Y338
ID Q9Y338 PRELIMINARY; PRT; 684 AA.
AC Q9Y338;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE SH3P12 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RA Lin W.S., Chuang L.M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF136380; AAD27647.1; -.
DR HSSP: Q60631; IGBO.
DR InterPro: IPR00108; -.
DR InterPro: IPR001452; -.
DR InterPro: IPR003127; -.
DR Pfam: PF00018; SH3; 3.
DR Pfam: PF02208; Sorb; 1.
DR PRINTS: PR00499; P67PHOX.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PSS0002; SH3; 3.
DR SMART: SM00326; SH3; 1.
SQ SEQUENCE 684 AA; 76341 MW; 2274E632BB07329C CRC64;

Query Match 9 6%; Score 163; DB 4; Length 684;
Best Local Similarity 25.0%; Pred. NO. 2.8e-05;
Matches 67; Conservative 40; Mismatches 103; Indels 58; Gaps 12;

Qy 41 RDSSTSPGDVYLSVSENSRVSHYIINSSGPRPPVPPSPAQPPGVSPSRLIGDQEFDSL 100
Db 369 RESDGAQGD--LTSLENSQIYKSVLEGGVTPIQDLSGLKRPSSASTKNSESPRHF--I 424
Qy 101 PALLEPFIKIHLDITTLIEPVARSQSGVILKQEEAFYRALFDENGDEEDLPFKGD 160
Db 425 PA-----DYLEST---EEFIRRRHD-----DKEMRPARAKDFKAQTLKELPLQGD 468
Qy 161 ILIRDRPEEQWMAEDSEGRGMIPVYVEKYRPASASVSALIGNQEGSHPOPLGPE 220
Db 469 IVYIKQIDQDQWYEGE--HHGKVGIFRRTYIELLPPAK----- 505
Qy 221 PGYPAQPSVNTPLPNLQNGPIYARVIOKRVPNAYDKTALALEVGEVLYKTKINVSQW--E 279
Db 506 ---AQPKKLTPQVYLE---YGEAIKAFNFGDQVEMSFRRGERITLLR--QVDENWYE 556
Qy 280 GECNG--KRGHPFTTHVRLDQ---QNP 302
Db 557 GRIPGTSKQGIPTTYVDVIRPLVKNP 584

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